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RAW SEQUENCE LISTING

DATE: 05/15/2003

PATENT APPLICATION: US/09/935,366A

TIME: 08:46:29

Input Set : A:\US09935366A.raw

Output Set: N:\CRF4\05152003\I935366A.raw

SEQUENCE LISTING

1 (1) GENERAL INFORMATION:

- 2 (i) APPLICANT: Bazan, J. Fernando
- 3 (ii) TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
- 4 (iii) NUMBER OF SEQUENCES: 16
- 5 (iv) CORRESPONDENCE ADDRESS:

- 6 (A) ADDRESSEE: DNAX Research Institute
- 7 (B) STREET: 901 California Avenue
- 8 (C) CITY: Palo Alto
- 9 (D) STATE: California
- 10 (E) COUNTRY: USA
- 11 (F) ZIP: 94304-1104

ENTERED

12 (v) COMPUTER READABLE FORM:

- 13 (A) MEDIUM TYPE: Floppy disk
- 14 (B) COMPUTER: IBM PC compatible
- 15 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- 16 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

17 (vi) CURRENT APPLICATION DATA:

- C--> 18 (A) APPLICATION NUMBER: US/09/935,366A
- C--> 19 (B) FILING DATE: 22-Aug-2001
- 20 (C) CLASSIFICATION:

21 (vii) PRIOR APPLICATION DATA:

- 22 (A) APPLICATION NUMBER: 09/122,443
- 23 (B) FILING DATE:

24 (viii) ATTORNEY/AGENT INFORMATION:

- 25 (A) NAME: Ching, Edwin P.
- 26 (B) REGISTRATION NUMBER: 34,090
- 27 (C) REFERENCE/DOCKET NUMBER: DX0758K1

28 (ix) TELECOMMUNICATION INFORMATION:

- 29 (A) TELEPHONE: (650)852-9196
- 30 (B) TELEFAX: (650)496-1200

31 (2) INFORMATION FOR SEQ ID NO: 1:

32 (i) SEQUENCE CHARACTERISTICS:

- 33 (A) LENGTH: 570 base pairs
- 34 (B) TYPE: nucleic acid
- 35 (C) STRANDEDNESS: single
- 36 (D) TOPOLOGY: linear

37 (ii) MOLECULE TYPE: cDNA

38 (ix) FEATURE:

- 39 (A) NAME/KEY: CDS
- 40 (B) LOCATION: 1..567

41 (ix) FEATURE:

- 42 (A) NAME/KEY: mat_peptide

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43      (B) LOCATION: 64..567
44      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
45      ATG CTG GGG AGC AGA GCT GTA ATG CTG CTG TTG CTG CTG CCC TGG ACA      48
46      Met Leu Gly Ser Arg Ala Val Met Leu Leu Leu Leu Leu Pro Trp Thr
47      -21 -20      -15      -10
48      GCT CAG GGC AGA GCT GTG CCT GGG GGC AGC AGC CCT GCC TGG ACT CAG      96
49      Ala Gln Gly Arg Ala Val Pro Gly Gly Ser Ser Pro Ala Trp Thr Gln
50      -5      1      5      10
51      TGC CAG CAG CTT TCA CAG AAG CTC TGC ACA CTG GCC TGG AGT GCA CAT      144
52      Cys Gln Gln Leu Ser Gln Lys Leu Cys Thr Leu Ala Trp Ser Ala His
53      15      20      25
54      CCA CTA GTG GGA CAC ATG GAT CTA AGA GAA GAG GGA GAT GAA GAG ACT      192
55      Pro Leu Val Gly His Met Asp Leu Arg Glu Glu Gly Asp Glu Glu Thr
56      30      35      40
57      ACA AAT GAT GTT CCC CAT ATC CAG TGT GGA GAT GGC TGT GAC CCC CAA      240
58      Thr Asn Asp Val Pro His Ile Gln Cys Gly Asp Gly Cys Asp Pro Gln
59      45      50      55
60      GGA CTC AGG GAC AAC AGT CAG TTC TGC TTG CAA AGG ATC CAC CAG GGT      288
61      Gly Leu Arg Asp Asn Ser Gln Phe Cys Leu Gln Arg Ile His Gln Gly
62      60      65      70      75
63      CTG ATT TTT TAT GAG AAG CTG CTA GGA TCG GAT ATT TTC ACA GGG GAG      336
64      Leu Ile Phe Tyr Glu Lys Leu Leu Gly Ser Asp Ile Phe Thr Gly Glu
65      80      85      90
66      CCT TCT CTG CTC CCT GAT AGC CCT GTG GCG CAG CTT CAT GCC TCC CTA      384
67      Pro Ser Leu Leu Pro Asp Ser Pro Val Ala Gln Leu His Ala Ser Leu
68      95      100      105
69      CTG GGC CTC AGC CAA CTC CTG CAG CCT GAG GGT CAC CAC TGG GAG ACT      432
70      Leu Gly Leu Ser Gln Leu Leu Gln Pro Glu Gly His His Trp Glu Thr
71      110      115      120
72      CAG CAG ATT CCA AGC CTC AGT CCC AGC CAG CCA TGG CAG CGT CTC CTT      480
73      Gln Gln Ile Pro Ser Leu Ser Pro Ser Gln Pro Trp Gln Arg Leu Leu
74      125      130      135
75      CTC CGC TTC AAA ATC CTT CGC AGC CTC CAG GCC TTT GTG GCT GTA GCC      528
76      Leu Arg Phe Lys Ile Leu Arg Ser Leu Gln Ala Phe Val Ala Val Ala
77      140      145      150      155
78      GCC CGG GTC TTT GCC CAT GGA GCA GCA ACC CTG AGT CCC TAA      570
79      Ala Arg Val Phe Ala His Gly Ala Ala Thr Leu Ser Pro
80      160      165
82 (2) INFORMATION FOR SEQ ID NO: 2:
83      (i) SEQUENCE CHARACTERISTICS:
84          (A) LENGTH: 189 amino acids
85          (B) TYPE: amino acid
86          (D) TOPOLOGY: linear
87      (ii) MOLECULE TYPE: protein
88      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
89      Met Leu Gly Ser Arg Ala Val Met Leu Leu Leu Leu Leu Pro Trp Thr
90      -21 -20      -15      -10
91      Ala Gln Gly Arg Ala Val Pro Gly Gly Ser Ser Pro Ala Trp Thr Gln
92      -5      1      5      10

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93   Cys Gln Gln Leu Ser Gln Lys Leu Cys Thr Leu Ala Trp Ser Ala His
94           15                20                25
95   Pro Leu Val Gly His Met Asp Leu Arg Glu Glu Gly Asp Glu Glu Thr
96           30                35                40
97   Thr Asn Asp Val Pro His Ile Gln Cys Gly Asp Gly Cys Asp Pro Gln
98           45                50                55
99   Gly Leu Arg Asp Asn Ser Gln Phe Cys Leu Gln Arg Ile His Gln Gly
100          60                65                70                75
101   Leu Ile Phe Tyr Glu Lys Leu Leu Gly Ser Asp Ile Phe Thr Gly Glu
102           80                85                90
103   Pro Ser Leu Leu Pro Asp Ser Pro Val Ala Gln Leu His Ala Ser Leu
104           95                100               105
105   Leu Gly Leu Ser Gln Leu Leu Gln Pro Glu Gly His His Trp Glu Thr
106          110               115               120
107   Gln Gln Ile Pro Ser Leu Ser Pro Ser Gln Pro Trp Gln Arg Leu Leu
108          125               130               135
109   Leu Arg Phe Lys Ile Leu Arg Ser Leu Gln Ala Phe Val Ala Val Ala
110          140               145               150               155
111   Ala Arg Val Phe Ala His Gly Ala Ala Thr Leu Ser Pro
112           160               165

114 (2) INFORMATION FOR SEQ ID NO: 3:
115   (i) SEQUENCE CHARACTERISTICS:
116       (A) LENGTH: 1203 base pairs
117       (B) TYPE: nucleic acid
118       (C) STRANDEDNESS: single
119       (D) TOPOLOGY: linear
120   (ii) MOLECULE TYPE: cDNA
121   (ix) FEATURE:
122       (A) NAME/KEY: CDS
123       (B) LOCATION: 113..700
124   (ix) FEATURE:
125       (A) NAME/KEY: mat_peptide
126       (B) LOCATION: 176..700
127   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
128   CGCTTAGAAG TCGGACTACA GAGTTAGACT CAGAACCAAA GGAGGTGGAT AGGGGGTCCA      60
129   CAGGCCTGGT GCAGATCACA GAGCCAGCCA GATCTGAGAA GCAGGGAACA AG ATG      115
130                                     Met
131                                     -21
132   CTG GAT TGC AGA GCA GTA ATA ATG CTA TGG CTG TTG CCC TGG GTC ACT      163
133   Leu Asp Cys Arg Ala Val Ile Met Leu Trp Leu Leu Pro Trp Val Thr
134   -20                -15                -10                -5
135   CAG GGC CTG GCT GTG CCT AGG AGT AGC AGT CCT GAC TGG GCT CAG TGC      211
136   Gln Gly Leu Ala Val Pro Arg Ser Ser Ser Pro Asp Trp Ala Gln Cys
137           1                5                10
138   CAG CAG CTC TCT CGG AAT CTC TGC ATG CTA GCC TGG AAC GCA CAT GCA      259
139   Gln Gln Leu Ser Arg Asn Leu Cys Met Leu Ala Trp Asn Ala His Ala
140          15                20                25
141   CCA GCG GGA CAT ATG AAT CTA CTA AGA GAA GAA GAG GAT GAA GAG ACT      307
142   Pro Ala Gly His Met Asn Leu Leu Arg Glu Glu Glu Asp Glu Glu Thr

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143	30	35	40	
144	AAA AAT AAT GTG CCC CGT ATC CAG TGT GAA GAT GGT TGT GAC CCA CAA	355		
145	Lys Asn Asn Val Pro Arg Ile Gln Cys Glu Asp Gly Cys Asp Pro Gln			
146	45 50 55 60			
147	GGA CTC AAG GAC AAC AGC CAG TTC TGC TTG CAA AGG ATC CGC CAA GGT	403		
148	Gly Leu Lys Asp Asn Ser Gln Phe Cys Leu Gln Arg Ile Arg Gln Gly			
149	65 70 75			
150	CTG GCT TTT TAT AAG CAC CTG CTT GAC TCT GAC ATC TTC AAA GGG GAG	451		
151	Leu Ala Phe Tyr Lys His Leu Leu Asp Ser Asp Ile Phe Lys Gly Glu			
152	80 85 90			
153	CCT GCT CTA CTC CCT GAT AGC CCC ATG GAG CAA CTT CAC ACC TCC CTA	499		
154	Pro Ala Leu Leu Pro Asp Ser Pro Met Glu Gln Leu His Thr Ser Leu			
155	95 100 105			
156	CTA GGA CTC AGC CAA CTC CTC CAG CCA GAG GAT CAC CCC CGG GAG ACC	547		
157	Leu Gly Leu Ser Gln Leu Leu Gln Pro Glu Asp His Pro Arg Glu Thr			
158	110 115 120			
159	CAA CAG ATG CCC AGC CTG AGT TCT AGT CAG CAG TGG CAG CGC CCC CTT	595		
160	Gln Gln Met Pro Ser Leu Ser Ser Ser Gln Gln Trp Gln Arg Pro Leu			
161	125 130 135 140			
162	CTC CGT TCC AAG ATC CTT CGA AGC CTC CAG GCC TTT TTG GCC ATA GCT	643		
163	Leu Arg Ser Lys Ile Leu Arg Ser Leu Gln Ala Phe Leu Ala Ile Ala			
164	145 150 155			
165	GCC CGG GTC TTT GCC CAC GGA GCA GCA ACT CTG ACT GAG CCC TTA GTG	691		
166	Ala Arg Val Phe Ala His Gly Ala Ala Thr Leu Thr Glu Pro Leu Val			
167	160 165 170			
168	CCA ACA GCT TAAGGATGCC CAGGTTCCCA TGGCTACCAT GATAAGACTA	740		
169	Pro Thr Ala			
170	175			
171	ATCTATCAGC CCAGACATCT ACCAGTTAAT TAACCCATTA GGA CTTGTGC TGTTCTTGTT	800		
172	TCGTTTGTTT TGCGTGAAGG GCAAGGACAC CATTATTAAA GAGAAAAGAA ACAAACCCCA	860		
173	GAGCAGGCAG CTGGCTAGAG AAAGGAGCTG GAGAAGAAGA ATAAAGTCTC GAGCCCTTGG	920		
174	CCTTGGAAGC GGGCAAGCAG CTGCGTGGCC TGAGGGGAAG GGGGCGGTGG CATCGAGAAA	980		
175	CTGTGAGAAA ACCCAGAGCA TCAGAAAAAG TGAGCCCAGG CTTTGCCCAT TATCTGTAAG	1040		
176	AAAAACAAGA AAAGGGGAAC ATTATACTTT CCTGGGTGGC TCAGGGAAAT GTGCAGATGC	1100		
177	ACAGTACTCC AGACAGCAGC TCTGTACCTG CCTGCTCTGT CCCTCAGTTC TAACAGAATC	1160		
178	TAGTCACTAA GAACTAACAG GACTACCAAT ACGAACTGAC AAA	1203		
180	(2) INFORMATION FOR SEQ ID NO: 4:			
181	(i) SEQUENCE CHARACTERISTICS:			
182	(A) LENGTH: 196 amino acids			
183	(B) TYPE: amino acid			
184	(D) TOPOLOGY: linear			
185	(ii) MOLECULE TYPE: protein			
186	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:			
187	Met Leu Asp Cys Arg Ala Val Ile Met Leu Trp Leu Leu Pro Trp Val			
188	-21 -20 -15 -10			
189	Thr Gln Gly Leu Ala Val Pro Arg Ser Ser Ser Pro Asp Trp Ala Gln			
190	-5 1 5 10			
191	Cys Gln Gln Leu Ser Arg Asn Leu Cys Met Leu Ala Trp Asn Ala His			
192	15 20 25			

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193   Ala Pro Ala Gly His Met Asn Leu Leu Arg Glu Glu Glu Asp Glu Glu
194           30                      35                      40
195   Thr Lys Asn Asn Val Pro Arg Ile Gln Cys Glu Asp Gly Cys Asp Pro
196           45                      50                      55
197   Gln Gly Leu Lys Asp Asn Ser Gln Phe Cys Leu Gln Arg Ile Arg Gln
198           60                      65                      70                      75
199   Gly Leu Ala Phe Tyr Lys His Leu Leu Asp Ser Asp Ile Phe Lys Gly
200           80                      85                      90
201   Glu Pro Ala Leu Leu Pro Asp Ser Pro Met Glu Gln Leu His Thr Ser
202           95                      100                     105
203   Leu Leu Gly Leu Ser Gln Leu Leu Gln Pro Glu Asp His Pro Arg Glu
204           110                     115                     120
205   Thr Gln Gln Met Pro Ser Leu Ser Ser Ser Gln Gln Trp Gln Arg Pro
206           125                     130                     135
207   Leu Leu Arg Ser Lys Ile Leu Arg Ser Leu Gln Ala Phe Leu Ala Ile
208           140                     145                     150                     155
209   Ala Ala Arg Val Phe Ala His Gly Ala Ala Thr Leu Thr Glu Pro Leu
210           160                     165                     170
211   Val Pro Thr Ala
212           175

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214 (2) INFORMATION FOR SEQ ID NO: 5:

215 (i) SEQUENCE CHARACTERISTICS:

216 (A) LENGTH: 102 amino acids

217 (B) TYPE: amino acid

218 (C) STRANDEDNESS: Not Relevant

219 (D) TOPOLOGY: linear

220 (ii) MOLECULE TYPE: peptide

221 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

```

222   Ser Cys Leu Gln Arg Ile His Gln Gly Leu Val Phe Tyr Glu Lys Leu
223       1                      5                      10                      15
224   Leu Gly Ser Asp Ile Phe Thr Gly Glu Pro Ser Leu His Pro Asp Gly
225           20                      25                      30
226   Ser Val Gly Gln Leu His Ala Ser Leu Leu Gly Leu Arg Gln Leu Leu
227           35                      40                      45
228   Gln Pro Glu Gly His His Trp Glu Thr Glu Gln Thr Pro Ser Pro Ser
229           50                      55                      60
230   Pro Ser Gln Pro Trp Gln Arg Leu Leu Leu Arg Leu Lys Ile Leu Arg
231           65                      70                      75                      80
232   Ser Leu Gln Ala Phe Val Ala Val Ala Ala Arg Val Phe Ala His Gly
233           85                      90                      95
234   Ala Ala Thr Leu Ser Gln
235           100

```

237 (2) INFORMATION FOR SEQ ID NO: 6:

238 (i) SEQUENCE CHARACTERISTICS:

239 (A) LENGTH: 174 amino acids

240 (B) TYPE: amino acid

241 (C) STRANDEDNESS: Not Relevant

242 (D) TOPOLOGY: linear

243 (ii) MOLECULE TYPE: peptide

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/935,366A

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Input Set : A:\US09935366A.raw

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L:18 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:19 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]